10 / 51050 4

SEQUENCE LISTING

- <110> Evotec NeuroSciences GmbH
- <120> Diagnostic and therapeutic use of Vault polynucleotides and proteins for neurodegenerative diseases.
- <130> P67785US1
- <140> PCT/EP03/03626
- <141> 2002-04-08
- <150> 02007820.0
- <151> 2002-04-08
- <150> US 60/370,214
- <151> 2002-04-08
- <160> 14
- <170> PatentIn Ver. 2.1
- <210> 1
- <211> 35
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence: ADPRTL1 cDNA
 fragment
- <400> 1

aatctaggaa tattccctgg gcttttgagg caatc

35

- <210> 2
- <211> 1724
- <212> PRT
- <213> Homo sapiens
- <400> 2
- Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys

 1 10 15
- Tyr Leu Pro Gln Gln Gln Lys Lys Leu Gln Thr Asp Ile Lys Glu 20 25 30
- Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile
- Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile 50 55 60
- Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser 65 70 75 80
- Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys
 85 90 95
- Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Glu

100	105	110

Val	Lys	Thr 115	GIu	GIA	Leu	Cys	Pro 120	Asp	Ser	Ala	Thr	G1u 125	Glu	Glu	Asp
Thr	Val 130	Glu	Leu	Thr	Glu	Phe 135	Gly	Met	Gln	Asn	Val 140	Glu	Ile	Pro	His
Leu 145	Pro	Gln	Asp	Phe	Glu 150	Val	Ala	Lys	Tyr	Asn 155	Thr	Leu	Glu	Lys	Val
Gly	Met	Glu	Gly	Gly 165	Gln	Glu	Ala	Val	Val 170	Val	Glu	Leu	Gln	Cys 175	Ser
Arg	Asp	Ser	Arg 180	Asp	Cys	Pro	Phe	Leu 185	Ile	Ser	Ser	His	Phe 190	Leu	Leu
Asp	Asp	Gly 195	Met	Glu	Thr	Arg	Arg 200	Gln	Phe	Ala	Ile	Lys 205	Lys	Thr	Ser
Glu	Asp 210	Ala	Ser	Glu	Tyr	Phe 215	Glu	Asn	Tyr	Ile	Glu 220	Glu	Leu	Lys	Lys
Gln 225	Gly	Phe	Leu	Leu	Arg 230	Glu	His	Phe	Thr	Pro 235	Glu	Ala	Thr	Gln	Leu 240
Ala	Ser	Glu	Gln	Leu 245	Gln	Ala	Leu	Leu	Leu 250	Glu	Glu	Val	Met	Asn 255	Ser
Ser	Thr	Leu	Ser 260	Gln	Glu	Val	Ser	Asp 265	Leu	Val	Glu	Met	Ile 270	Trp	Ala
Glu	Ala	Leu 275	Gly	His	Leu	Glu	His 280	Met	Leu	Leu	Lys	Pro 285	Val	Asn	Arg
Ile	Ser 290	Leu	Asn	Asp	Val	Ser 295	Lys	Ala	Glu	Gly	Ile 300	Leu	Leu	Leu	Val
Lys 305	Ala	Ala	Leu	Lys	Asn 310	Gly	Glu	Thr	Ala	Glu 315	Gln	Leu	Gln	Lys	Met 320
Met	Thr	Glu	Phe	Tyr 325	Arg	Leu	Ile	Pro	His 330	Lys	Gly	Thr	Met	Pro 335	Lys
Glu	Val	Asn	Leu 340	Gly	Leu	Leu	Ala	Lys 345	Lys	Ala	Asp	Leu	Cys 350	Gln	Lev
Ile	Arg	Asp 355	Met	Val	Asn	Val	Cys 360	Glu	Thr	Asn	Leu	Ser 365	Lys	Pro	Asr
Pro	Pro 370	Ser	Leu	Ala	Lys	Tyr 375	Arg	Ala	Leu	Arg	Cys 380	Lys	Ile	Glu	His
Val 385	Glu	Gln	Asn	Thr	Glu 390	Glu	Phe	Leu	Arg	Val 395	Arg	Lys	Glu	Val	Let 400
Gln	Asn	His	His	Ser 405	Lys	Ser	Pro	Val	Asp 410	Val	Leu	Gln	Ile	Phe 415	Arg
นาไ	C1.,	7 ~~	1707	7 an	Clu	Thr	Thr	C1.,	Dho	Ton	cor	Tare	LON	Clar	λαν

Val	Arg	Pro 435	Leu	Leu	His	Gly	Ser 440	Pro	Val	Gln	Asn	Ile 445	Val	Gly	Ile
Leu	Cys 450	Arg	Gly	Leu	Leu	Leu 455	Pro	Lys	Val	Val	Glu 460	Asp	Arg	Gly	Val
Gln 465	Arg	Thr	Asp	Val	Gly 470	Asn	Leu	Gly	Ser	Gly 475	Ile	Tyr	Phe	Ser	Asp 480
Ser	Leu	Ser	Thr	Ser 485	Ile	Lys	Tyr	Ser	His 490	Pro	Gly	Glu	Thr	Asp 495	Gly
Thr	Arg	Leu	Leu 500	Leu	Ile	Cys	Asp	Val 505	Ala	Leu	Gly	Lys	Cys 510	Met	Asp
Leu	His	Glu 515	Lys	Asp	Phe	Ser	Leu 520	Thr	Glu	Ala	Pro	Pro 525	Gly	Tyr	Asp
Ser	Val 530	His	Gly	Val	Ser	Gln 535	Thr	Ala	Ser	Val	Thr 540	Thr	Asp	Phe	Glu
Asp 545	Asp	Glu	Phe	Val	Val 550	Tyr	Lys	Thr	Asn	Gln 555	Val	Lys	Met	Lys	Tyr 560
Ile	Ile	Lys	Phe	Ser 565	Met	Pro	Gly	Asp	Gln 570	Ile	Lys	Asp	Phe	His 575	Pro
Ser	Asp	His	Thr 580	Glu	Leu	Glu	Glu	Tyr 585	Arg	Pro	Glu	Phe	Ser 590	Asn	Phe
Ser	Lys	Val 595	Glu	Asp	Tyr	Gln	Leu 600	Pro	Asp	Ala	Lys	Thr 605	Ser	Ser	Ser
	610					615					620			Leu	
Asp 625	Val	His	Ile	Lys	Gly 630	Arg	Ile	Ile	Asp	Thr 635	Val	Ala	Gln	Val	Il∈ 640
				645			_		650					Ala 655	
			660					665					670	Glu	
Phe	Ile	Asn 675	Gly	Lys	His	Ile	Val 680	Gly	Glu	Ile	Lys	Glu 685	Lys	Glu	Glu
Ala	Gln 690	Gln	Glu	Tyr	Leu	Glu 695	Ala	Val	Thr	Gln	Gly 700	His	Gly	Ala	Tyr
705					710					715				Gly	720
Leu	Pro	Pro	Lys	Ala 725	Lys	Val	Leu	Ile	Lys 730	Ile	Thr	Tyr	Ile	Thr 735	Glu
Leu	Ser	Ile	Leu	Glv	Thr	Val	Glv	Val	Phe	Phe	Met	Pro	Ala	Thr	Val

Ala Pro Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser 790 795 Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile 810 Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His 820 825 Ile Gly Leu Ser Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His Pro Glu Lys Glu Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu 855 Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys 870 875 Leu Asp Cys Ser Ser Ser Met Glu Gly Val Thr Phe Leu Gln Ala Lys 890 885 Gln Ile Ala Leu His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val 905 Asn Ile Ile Gln Phe Gly Thr Gly Tyr Lys Glu Leu Phe Ser Tyr Pro 915 920 Lys His Ile Thr Ser Asn Thr Ala Ala Glu Phe Ile Met Ser Ala 935 Thr Pro Thr Met Gly Asn Thr Asp Phe Trp Lys Thr Leu Arg Tyr Leu 945 955 Ser Leu Leu Tyr Pro Ala Arg Gly Ser Arg Asn Ile Leu Leu Val Ser 970 Asp Gly His Leu Gln Asp Glu Ser Leu Thr Leu Gln Leu Val Lys Arg 985 Ser Arg Pro His Thr Arg Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala 1000 Asn Arg His Val Leu Arg Ile Leu Ser Gln Cys Gly Ala Gly Val Phe 1010 1015 Glu Tyr Phe Asn Ala Lys Ser Lys His Ser Trp Arg Lys Gln Ile Glu 1025 1030 1035 Asp Gln Met Thr Arg Leu Cys Ser Pro Ser Cys His Ser Val Ser Val 1045 1050

Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln Ala Pro

1060 1065 1070

- Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu Val Tyr Gly
 1075 1080 1085
- Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala Leu Ile Gln Glu 1090 1095 1100
- Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu Leu Gln Lys Thr Thr 1105 1110 1115 1120
- Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala Leu Ile Arg Asp Tyr
 1125 1130 1135
- Glu Asp Gly Ile Leu His Glu Asn Glu Thr Ser His Glu Met Lys Lys 1140 1145 1150
- Gln Thr Leu Lys Ser Leu Ile Ile Lys Leu Ser Lys Glu Asn Ser Leu 1155 1160 1165
- Ile Thr Gln Phe Thr Ser Phe Val Ala Val Glu Lys Arg Asp Glu Asn 1170 1175 1180
- Glu Ser Pro Phe Pro Asp Ile Pro Lys Val Ser Glu Leu Ile Ala Lys 1185 1190 1195 1200
- Glu Asp Val Asp Phe Leu Pro Tyr Met Ser Trp Gln Gly Glu Pro Gln
 1205 1210 1215
- Glu Ala Val Arg Asn Gln Ser Leu Leu Ala Ser Ser Glu Trp Pro Glu 1220 1225 1230
- Leu Arg Leu Ser Lys Arg Lys His Arg Lys Ile Pro Phe Ser Lys Arg 1235 1240 1245
- Lys Met Glu Leu Ser Gln Pro Glu Val Ser Glu Asp Phe Glu Glu Asp 1250 1255 1260
- Gly Leu Gly Val Leu Pro Ala Phe Thr Ser Asn Leu Glu Arg Gly Gly 1265 1270 1275 1280
- Val Glu Lys Leu Leu Asp Leu Ser Trp Thr Glu Ser Cys Lys Pro Thr 1285 1290 1295
- Ala Thr Glu Pro Leu Phe Lys Lys Val Ser Pro Trp Glu Thr Ser Thr 1300 1305 1310
- Ser Ser Phe Phe Pro Ile Leu Ala Pro Ala Val Gly Ser Tyr Leu Thr
 1315 1320 1325
- Pro Thr Thr Arg Ala His Ser Pro Ala Ser Leu Ser Phe Ala Ser Tyr 1330 1335 1340
- Arg Gln Val Ala Ser Phe Gly Ser Ala Ala Pro Pro Arg Gln Phe Asp 1345 1350 1355 1360
- Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly Thr Cys Ala Asp Trp
 1365 1370 1375
- Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly Pro Pro Gln Asn Pro Pro

1380 1385 1390

- Ser Ala Pro Tyr Cys Gly Ile Val Phe Ser Gly Ser Ser Leu Ser Ser 1395 1400 1405
- Ala Gln Ser Ala Pro Leu Gln His Pro Gly Gly Phe Thr Thr Arg Pro 1410 1415 1420
- Ser Ala Gly Thr Phe Pro Glu Leu Asp Ser Pro Gln Leu His Phe Ser 1425 1430 1435 1440
- Leu Pro Thr Asp Pro Asp Pro Ile Arg Gly Phe Gly Ser Tyr His Pro
 1445 1450 1455
- Ser Ala Tyr Ser Pro Phe His Phe Gln Pro Ser Ala Ala Ser Leu Thr 1460 1465 1470
- Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys 1475 1480 1485
- Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser 1490 1495 1500
- Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser 1505 1510 1515 1520
- Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys 1525 1530 1535
- Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe 1540 1545 1550
- Leu Glu Val Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln 1555 1560 1565
- Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly
 1570 1575 1580
- Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr 1585 1590 1595 1600
- Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly
 1605 1610 1615
- Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val 1620 1625 1630
- Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys 1635 1640 1645
- Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp 1650 1660
- Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu 1665 1670 1675 1680
- Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp
 1685 1690 1695
- Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val

Ser	Pro	Leu	His	Arg	Val	Leu	His	Tyr	Ser	Gln	Gly
		1715					1720				

<210> 3 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: primer for the human ADPRTL1 gene	
<400> 3 gatgctgtgc cttggacaga a	21
<210> 4 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: primer for the human ADPRTL1 gene	
<400> 4 tggtgtaagt ttccagaagc ca	22
<210> 5 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: primer for cyclophilin B gene	
<400> 5 actgaagcac tacgggcctg	20
<210> 6 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: primer for cyclophilin B gene	
<400> 6 agccgttggt gtctttgcc	19

<210> 7 <211> 20

<212> <213>	DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: primer for the ribosomal protein S9 gene	
<400> ggtcaa	7 aattt accctggcca	20
<210><211><211><212><213>	22	
<220> <223>	Description of Artificial Sequence: primer for the ribosomal protein S9 gene	
<400> tctcat	8 ccaag cgtcagcagt tc	22
<210><211><211><212><213>	19	
<220> <223>	Description of Artificial Sequence: primer for the beta-actin gene	
<400> tggaad	9 Eggtg aaggtgaca	19
<210><211><211><212><213>	19	
<220> <223>	Description of Artificial Sequence: primer for the beta-actin gene	
<400> ggcaag	10 gggac ttcctgtaa	19
<210><211><211><212><213>	20	
<220> <223>	Description of Artificial Sequence: primer for the GAPDH gene	
<400>	11	20

<210>	12	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
	Description of Artificial Sequence: primer for the GAPDH gene	
<400>		
gctaag	cagt tggtggtgca g	21
<210>	13	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
	Description of Artificial Sequence: primer for the transferrin receptor (TRR) gene	
<400>	13	
gtcgct	ggtc agttcgtgat t	21
<210>	14	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
	Description of Artificial Sequence: primer for the transferrin receptor (TRR) gene	
<400>	14	
agcagt	tggc tgttgtacct ctc	23